<212> PRT

## SEQUENCE LISTING

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<110> Allen, Keith D.
      Matthews, William
      Moore, Mark
<120> TRANSGENIC MICE CONTAINING FPR-RS4 GENE
  DISRUPTIONS
<130> R-632
<140> To Be Assigned
<141> 2001-12-04
<150> US 60/251,817
<151> 2000-12-06
<150> US 60/311,056
<151> 2001-08-08
<160> 4
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 1554
<212> DNA
<213> Mus musculus
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ccagtgttet cetecteatg gtaateteat geetetacaa tetacateca gtacactete 120
aggtcaacat cagagtaagg atatggagcc taggatccct tcttaaacaa ctggagacgt 180
aataaccctc tttattaatg catagaatta agatttccat agggatattt aacagaaaac 240
cacatttact ctattacccc tagaataggt acttttaaat agaaggtgat gtgggatctg 300
aggtaggcgg gacaagaatg gagacacatc tgaaaaatag ttattgttga aaatttttag 360
gtactgacaa gatggaagtc aacatttcaa tgcctctgaa tggatcagaa gttgtgtttt 420
atgattctac cacctcaagt gttctatgga tcctctcatt agtggttctc tttataacct 480
ttgtcctcgg tgttctaggt aatgggcttg tgatttgggt ggctgggttc cagatggcac 540
acactgtgac cactgtctct tatctgaact tggctttgag tgatttatct ttcatggtta 600
ctctaccact tcacatcatc tcaatggtca tgagaggaaa atggcttttt ggttggtttc 660
tttgcaaatt agttcacata attgcaaaca taaacctttt tgtaagtatc ttcctaatca 720
ctcttattgc catggategc tgtatttgtg tcctgtgccc agtatggtct cagaatcacc 780
gaactgtgag tetggecaga aaagtggtte ttggagettg gatatttget etgetgetta 840
cettgecaca ttttetette ttgactacag tgagagatge aagaggggat gtgtactgta 900
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ctgccacage ttcaggaate atcaatttca ttattggatt cagcatgccc atgtctttca 1020
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 gtcgtccttt acgtgtcctc actgctgtag cgatttcctt ctttgtctgt tggttccctt 1140
ttcaattaat tatgetttta ggcaacatet ttaacaatga gacactgage attattcata 1200
 tgttggttaa cccagcaaat accttggctt cctttaacag ctgcctcaac ccaatactct 1260
 atgtattcct gggtcaggaa ttcagagaca gactaatcta ttctctgtat gccagtctag 1320
 agagggccct gagggaagac tagtccttga tggaaaattc agtcctgagc actgacacag 1380
 acagcaactt gtetteatga actgeagact etgagetata ggaaatggea ggagtaagge 1440
 caatgggatt tttttttccc taccctagtc ttaatttctg tcttatccta tcttgcatga 1500
 aatttctgag tataactata gaatctctct gattctgatt tggaagacag aagt
 <210> 2
 <211> 323
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## <213> Mus musculus

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<400> 2
Met Glu Val Asn Ile Ser Met Pro Leu Asn Gly Ser Glu Val Val Phe
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Tyr Asp Ser Thr Thr Ser Ser Val Leu Trp Ile Leu Ser Leu Val Val
                                25
Leu Phe Ile Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile
Trp Val Ala Gly Phe Gln Met Ala His Thr Val Thr Thr Val Ser Tyr
                        55
Leu Asn Leu Ala Leu Ser Asp Leu Ser Phe Met Val Thr Leu Pro Leu
                    7.0
                                        75
His Ile Ile Ser Met Val Met Arg Gly Lys Trp Leu Phe Gly Trp Phe
                                    90
                85
Leu Cys Lys Leu Val His Ile Ile Ala Asn Ile Asn Leu Phe Val Ser
            100
                                105
Ile Phe Leu Ile Thr Leu Ile Ala Met Asp Arg Cys Ile Cys Val Leu
                            120
                                                125
Cys Pro Val Trp Ser Gln Asn His Arg Thr Val Ser Leu Ala Arg Lys
                        135
                                           140
    130
Val Val Leu Gly Ala Trp Ile Phe Ala Leu Leu Leu Thr Leu Pro His
                    150
                                        155
Phe Leu Phe Leu Thr Thr Val Arg Asp Ala Arg Gly Asp Val Tyr Cys
                                    170
                                                        175
                165
Ile Ser Lys Phe Glu Ser Trp Val Ala Thr Ser Glu Glu Gln Leu Lys
                                                    190
                                185
            180
Met Ser Val Ile Ala Ala Thr Ala Ser Gly Ile Ile Asn Phe Ile Ile
                                                205
                            200
        195
Gly Phe Ser Met Pro Met Ser Phe Ile Ala Ile Cys Tyr Gly Leu Met
                        215
                                            220
    210
Ala Ala Lys Ile Cys Arg Arg Gly Phe Val Asn Ser Ser Arg Pro Leu
                                        235
                    230
Arg Val Leu Thr Ala Val Ala Ile Ser Phe Phe Val Cys Trp Phe Pro
                                    250
                 245
Phe Gln Leu Ile Met Leu Leu Gly Asn Ile Phe Asn Asn Glu Thr Leu
                                265
            260
Ser Ile Ile His Met Leu Val Asn Pro Ala Asn Thr Leu Ala Ser Phe
                             280
Asn Ser Cys Leu Asn Pro Ile Leu Tyr Val Phe Leu Gly Gln Glu Phe
                         295
                                            300
Arg Asp Arg Leu Ile Tyr Ser Leu Tyr Ala Ser Leu Glu Arg Ala Leu
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305
                     310
Arg Glu Asp
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<210> 3
<211> 200
<212> DNA
<213> Artificial Sequence
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tagaataggt actttttaaa atagaaggt atgtgggatc tgaggtaagg cgggacaaga 120
tggagacaca tctgaaaat agttattgtt gaaaattttt aggtgctgac aagatggaag 180
tcaacatttc aatgcctctg

<sup>&</sup>lt;220> <223> Targeting Vector

- <210> 4
- <211> 200
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Targeting Vector

ccatggatcg ctgtatttgt

<400> 4

ceactgtete ttatetgaac ttggetttga gtgatttate tttcatgget actetaceae 60 ttcacatcat ctcaatggtc atgagaggaa aatggctttt tggttggttt ctttgcaaat 120 tagttcacat aattgcaaac ataaaccttt ttgtaagtat cttcctaatc actcttattg 180

200